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APPLICATION NUMBER	FILING/RECEIPT DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NUMBER
09/873,881	06/04/2001	Fred W. Scott	18617.NEW

CONFIRMATION NO. 6373
FORMALITIES LETTER



OC000000006309437

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 Suite 2000
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Date Mailed: 07/18/2001

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS
 CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE
 DISCLOSURES**

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

For questions regarding compliance to these requirements, please contact:

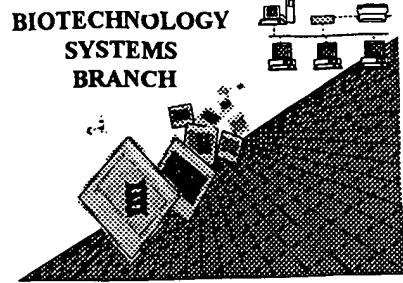
- For Rules Interpretation, call (703) 308-4216
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PART 3 - OFFICE COPY

RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/873,881

Source: O1PE

Date Processed by STIC: 6/21/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/873,881</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Acid	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input checked="" type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:36

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Scott, Fred W.
5 <120> TITLE OF INVENTION: Recombinant Multivalent Viral Vaccine
7 <130> FILE REFERENCE: 18617.0016
9 <140> CURRENT APPLICATION NUMBER: US/09/873,881
11 <141> CURRENT FILING DATE: 2001-06-04
13 <160> NUMBER OF SEQ ID NOS: 25

ERRORED SEQUENCES

212 <210> SEQ ID NO: 2
214 <211> LENGTH: 1575
216 <212> TYPE: DNA
218 <213> ORGANISM: rabies virus
220 <220> FEATURE:
222 <223> OTHER INFORMATION:
E--> 224 <400> SEQUENCE: 2 <insert sequence number
225 atg gtt cct cag gct ctc ctg ttt gta ccc ctt ctg gtt ttt 42
226 Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe
W--> 227 1 5 10
229 cca ttg tgt ttt ggg aaa ttc cct att tac acg ata cta gac 84
230 Pro Leu Cys Phe Gly Lys Phe Pro Ile TYR Thr Ile Leu Asp
W--> 231 15 20 25
233 aag ctt ggt ccc tgg agc ccg att gac ata cat cac ctc agc 126
234 Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser
W--> 235 30 35 40
237 tgc cca aac aat ttg gta gtg gag gac gaa gga tgc acc aac 168
238 Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn
W--> 239 45 50 55
241 ctg tca ggg ttc tcc tac atg gaa ctt aaa gtt gga tac atc 210
242 Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
W--> 243 60 65 70
245 tta gcc ata aaa atg aac ggg ttc act tgc aca ggc gtt gtg 252
246 Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
W--> 247 75 80 85
249 acg gag gct gaa acc tac act aac ttc gtt ggt tat gtc aca 294
250 Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr
W--> 251 85 90 95
253 acc acg ttc aaa aga aag cat ttc cgc cca aca cca gat gca 336
254 Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
W--> 255 100 105 110
257 tgt aga gcc gcg tac aac tgg aag atg gcc ggt gac ccc aga 378
258 Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
W--> 259 115 120 125
261 tat gaa gag tct cta cac aat ccg tac cct gac tac cgc tgg 420

262 Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
W--> 263 130 135 140

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265	ctt	cga	act	gta	aaa	acc	acc	aag	gag	tct	ctc	gtt	atc	ata	462
266	Leu	Arg	Thr	Val	Lys	Thr	Thr	Lys	Glu	Ser	Leu	Val	Ile	Ile	
W--> 267				145				150							504
269	tct	cca	agt	gta	gca	gat	ttg	gac	cca	tat	gac	aga	tcc	ctt	
270	Ser	Pro	Ser	Val	Ala	Asp	Leu	Asp	Pro	Tyr	Asp	Arg	Ser	Leu	
W--> 271	155			160				165							546
273	cac	tcg	agg	gtc	tcc	cct	agc	ggg	aag	tgc	tca	gga	gta	gcg	
274	His	Ser	Arg	Val	Phe	Pro	Ser	Gly	Lys	Cys	Ser	Gly	Val	Ala	
W--> 275	170			175				180							588
277	gtg	tct	tct	acc	tac	tgc	tcc	act	aac	cac	gat	tac	acc	att	
278	Val	Ser	Ser	Thr	Tyr	Cys	Ser	Thr	Asn	His	Asp	Tyr	Thr	Ile	
W--> 279	185			190				195							630
281	tgg	atg	ccc	gag	aat	ccg	aga	cta	ggg	atg	tct	tgt	gac	att	
282	Trp	Met	Pro	Glu	Asn	Pro	Arg	Leu	Gly	Met	Ser	Cys	Asp	Ile	
W--> 283	200			205				210							672
285	ttt	acc	aat	agt	aga	ggg	aag	aga	gca	tcc	aaa	ggg	agt	gag	
286	Phe	Thr	Asn	Ser	Arg	Gly	Lys	Arg	Ala	Ser	Lys	Gly	Ser	Glu	
W--> 287	215			220											714
289	act	tgc	ggc	ttt	gta	gat	gaa	aga	ggc	cta	tat	aag	tct	tta	
290	Thr	Cys	Gly	Phe	Val	Asp	Glu	Arg	Gly	Leu	Tyr	Lys	Ser	Leu	
W--> 291	225			230				235							756
293	aaa	gga	gca	tgc	aaa	ctc	aag	tta	tgt	gga	gtt	cta	gga	ctt	
294	Lys	Gly	Ala	Cys	Lys	Leu	Lys	Leu	Cys	Gly	Val	Leu	Gly	Leu	
W--> 295	240			245				250							798
297	aga	ctt	atg	gat	gga	aca	tgg	gtc	gcg	atg	caa	aca	tca	aat	
298	Arg	Leu	Met	Asp	Gly	Thr	Trp	Val	Ala	Met	Gln	Thr	Ser	Asn	
W--> 299	255			260				265							840
301	gaa	acc	aaa	tgg	tgc	gct	ccc	gat	cag	ttg	gtg	aac	ctg	cac	
302	Glu	Thr	Lys	Trp	Cys	Pro	Pro	Asp	Gln	Leu	Val	Asn	Leu	His	
W--> 303	270			275				280							882
305	gac	ttt	cgc	tca	gac	gaa	att	gag	cac	ctt	gtt	gta	gag	gag	
306	Asp	Phe	Arg	Ser	Asp	Glu	Ile	Glu	His	Leu	Val	Val	Glu	Glu	
W--> 307	285			290											924
309	ttg	gtc	agg	aag	aga	gag	gag	tgt	ctg	gat	gca	cta	gag	tcc	
W--> 310	Leu	Val	Arg	Lys	Arg	Glu	Glu	Cys	Leu	Asp	Ala	Leu	Glu	Ser	
W--> 311	295	→	Lys	300				305							966
313	atc	atg	aca	aac	aag	tca	gtg	agt	ttc	aga	cgt	ctc	agt	cat	
314	Ile	Met	Thr	Thr	Lys	Ser	Val	Ser	Phe	Arg	Arg	Leu	Ser	His	
W--> 315	310			315				320							1008
317	tta	aga	aaa	ctt	gtc	cct	ggg	ttt	gga	aaa	gca	tat	acc	ata	
318	Leu	Arg	Lys	Leu	Val	Pro	Gly	Phe	Gly	Lys	Ala	Tyr	Thr	Ile	
W--> 319	325			330				335							1050
321	ttc	aac	aag	acc	ttg	atg	gaa	gcc	gat	gct	cac	tac	aag	tca	
322	Phe	Asn	Lys	Thr	Leu	Met	Glu	Ala	Asp	Ala	His	Tyr	Lys	Ser	
W--> 323															1092
325	gtc	aga	act	tgg	aat	gag	atc	ctc	cct	tca	aaa	ggg	tgt	tta	345
326	Val	Arg	Thr	Trp	Asn	Glu	Ile	Leu	Pro	Ser	Lys	Gly	Cys	Leu	
W--> 327															1134
329	aga	gtt	ggg	ggg	agg	tgt	cat	cct	cat	gtg	aac	ggg	gtg	ttt	360

RAW SEQUENCE LISTING
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modified rev.

330	Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe			
W--> 331		365	370	
333	ttc aat ggt ata ata tta gga cct gac ggc aat gtc tta atc			
334	Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile			
W--> 335		380	385	390
337	cca gag atg caa tca tcc ctc ctc cag caa cat atg gag ttg			1218
338	Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu			
W--> 339		395	400	40
341	ttg gaa tcc tcg gtt atc ccc ctt gtg cac ccc ctg gca gac			1260
342	Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp			
W--> 343		410	415	
346	ccg tct acc gtt ttc aag gac ggt gac gag gct gag gat ttt			
347	Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe			
W--> 348		425	430	
350	gtt gaa gtt cac ctt ccc gat gtg cac aat cag gtc tca gga			1344
351	Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly			
W--> 352		435	440	445
354	gtt gac ttg ggt ctc ccg aac tgg ggg aag tat gta tta ctg			1386
355	Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu			
W--> 356		450	455	460
358	agt gca ggg gcc ctg act gcc ttg atg ttg ata att ttc ctg			1428
359	Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu			
W--> 360		465	470	47
362	atg aca tgt tgt aga aga gtc aat cga tca gaa cct acg caa			
363	Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln			
W--> 364		480	485	
366	cac aat ctc aga ggg aca ggg agg gag gtg tca gtc act ccc			1512
367	His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro			
W--> 368		495	500	
370	caa agc ggg aag atc ata tct tca tgg gaa tca cac aag agt			1554
371	Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser			
W--> 372		505	510	515
374	ggg ggt gag acc aga ctg tga 1575			
375	Gly Gly Glu Thr Arg Leu			
W--> 376		520		
379	<210> SEQ ID NO: 3			
381	<211> LENGTH: (44) 40 shown			
383	<212> TYPE: DNA			
385	<213> ORGANISM: P11 late promoter and leader sequence			
387	<220> FEATURE:			
389	<223> OTHER INFORMATION:			
E--> 391	<400> SEQUENCE: 3<			
E--> 392	taaaatata gtagaattt attttgttt ttctatgt			
394	<210> SEQ ID NO: 4			
396	<211> LENGTH: 28			
398	<212> TYPE: DNA			
400	<213> ORGANISM: artificial sequence			

← number the amino acids under every 5 amino acids

40 ← insert cumulative base total at right margin of each line

402 <220> FEATURE:
404 <223> OTHER INFORMATION: forward primer

RAW SEQUENCE LISTING
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E--> 406 <400> SEQUENCE: 4<

407 cgggatccat tttcccttcg tttgccat 28

410 <210> SEQ ID NO: 5

412 <211> LENGTH: 28

414 <212> TYPE: DNA

416 <213> ORGANISM: artificial sequence

W--> 418 <220> FEATURE: reverse primer move down to C2237 line - do not insert any
420 <223> OTHER INFORMATION:

E--> 422 <400> SEQUENCE: 5<

423 cgggtaccga tttctccgtg ataggtat 28

426 <210> SEQ ID NO: 6

428 <211> LENGTH: 18

430 <212> TYPE: DNA

432 <213> ORGANISM: artificial sequence

W--> 434 <220> FEATURE: sequencing primer move down to C2237 line - do not insert any
436 <223> OTHER INFORMATION:

E--> 438 <400> SEQUENCE: 6<

439 ctacttgcac agataggt 18

443 <210> SEQ ID NO: 7

445 <211> LENGTH: 2007

447 <212> TYPE: DNA

449 <213> ORGANISM: feline calicivirus

451 <220> FEATURE:

453 <223> OTHER INFORMATION:

E--> 455 <400> SEQUENCE: 1 7<

456 atg tgc tca acc tgc gct aac gtc ctt aaa tac tat gat tgg gat 45

457 Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp

W--> 458

1 5 10

460 cct cac atc aaa ttg gta atc aac ccc aac aaa ttt cta cat gtt 90

461 Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val

W--> 462

20 25

464 ggc ttc tgc gat aac cct tta atg tgt tat cct gaa tta cta 135

465 Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu

W--> 466

35 40

468 cct gaa ttt ggc acc atg tgg gat tgt gat caa tcg cca ctc caa 180

469 Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln

W--> 470

50 55

472 gtc tac ctt gag tca atc ctg ggt gat gat gaa tgg tcc tcc act 225

473 Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr

W--> 474

65 70

476 cat gaa gca att gac cca gtt gtg cca cca atg cat tgg gat gaa 270

477 His Glu Ala Ile Asp Pro Val Val Pro Met His Trp Asp Glu

W--> 478

80 85

480 gcc gga aaa atc ttc caa cca cac cct ggc gtc ctt atg cat cac 315

481 Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His

W--> 482

95 100

484 ctc atc tgt aag gtt gca gaa gga tgg gac cca aac ctg cca ctt
485 Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu
W--> 486

360

110

115

RAW SEQUENCE LISTING
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DATE: 06/21/2001
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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

*misaligned
as read and
noS.*

488	ttc	cgc	ttg	gaa	gct	gac	gat	ggt	tcc	atc	acg	aca	cct	gaa	cag	405
489	Phe	Arg	Leu	Glu	Ala	Asp	Asp	Gly	Ser	Ile	Thr	Thr	Pro	Glu	Gln	
W--> 490																
492	gga	aca	atg	gtt	ggt	gga	gtc	att	gct	gag	ccc	aac	gcc	caa	atg	125
493	Gly	Thr	Met	Val	Gly	Gly	Val	Ile	Ala	Glu	Pro	Asn	Ala	Gln	Met	450
W--> 494																
496	tca	acc	gca	gct	gac	atg	gcc	act	ggg	aaa	agt	gtg	gac	tct	gag	495
497	Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys	Ser	Val	Asp	Ser	Glu	
W--> 498																
500	tgg	gaa	gcc	ttc	ttc	tcc	ttt	cac	act	agt	gtg	aac	tgg	agc	aca	540
501	Trp	Glu	Ala	Phe	Phe	Ser	Phe	His	Thr	Ser	Val	Asn	Trp	Ser	Thr	
W--> 502																
504	tct	gaa	act	cag	ggg	aag	ata	ctc	ttt	aaa	caa	tcc	tta	gga	cca	585
505	Ser	Glu	Thr	Gln	Gly	Ile	Leu	Phe	Lys	Gln	Ser	Leu	Gly	Pro		
W--> 506																
508	ttg	ctc	aac	ccc	tac	ctt	acc	cat	ctt	gca	aag	ctg	tat	gtt	gct	630
509	Leu	Leu	Asn	Pro	Tyr	Leu	Thr	His	Leu	Ala	Lys	Leu	Tyr	Val	Ala	
W--> 510																
512	tgg	tct	ggt	tct	gtt	gat	gtt	agg	ttt	tct	att	tct	gga	tct	ggt	675
513	Trp	Ser	Gly	Ser	Val	Asp	Val	Arg	Phe	Ser	Ile	Ser	Gly	Ser	Gly	
W--> 514																
516	gtc	ttt	gga	ggg	aaa	tta	gct	att	gtt	gtg	ccg	cca	gga	att	720	
517	Val	Phe	Gly	Gly	Lys	Leu	Ala	Ala	Ile	Val	Val	Pro	Pro	Gly	Ile	
W--> 518																
520	gat	cct	gtt	caa	agt	act	tca	atg	ctg	caa	tat	cct	cat	gtc	ctc	765
521	Asp	Pro	Val	Gln	Ser	Thr	Met	Leu	Gln	Tyr	Pro	His	Val	Leu		
W--> 522																
524	ttt	gat	gct	cgt	caa	gtt	gaa	cct	gtt	atc	ttt	tcc	att	ccc	gat	810
525	Phe	Asp	Ala	Arg	Gln	Val	Glu	Pro	Val	Ile	Phe	Ser	Ile	Pro	Asp	
W--> 526																
528	cta	aga	agc	acc	tta	tat	cac	ctt	atg	tct	gac	act	gat	acc	aca	855
529	Leu	Arg	Ser	Thr	Leu	Tyr	His	Leu	Met	Ser	Asp	Thr	Asp	Thr	Thr	
W--> 530																
532	tcg	ttg	gta	atc	atg	gtg	tac	aat	gat	ctt	att	aac	ccc	tat	gct	900
533	Ser	Leu	Val	Ile	Met	Val	Tyr	Asn	Asp	Leu	Ile	Asn	Pro	Tyr	Ala	
W--> 534																
536	aat	gac	tca	aac	tct	tcg	ggc	tgc	att	gtc	act	gtg	gaa	act	aaa	945
537	Asn	Asp	Ser	Asn	Ser	Ser	Gly	Cys	Ile	Val	Thr	Val	Glu	Thr	Lys	
W--> 538																
540	ccg	ggg	cca	gat	ttc	aag	ttt	cac	ctc	tta	aaa	cct	cct	ggg	tct	990

541 Pro Gly Pro Asp Phe Lys His Leu Leu Lys Pro Pro Gly Ser			
W--> 542	320	325	
544 atg tta act cac gga tct atc cca tct gat cta atc cca aaa tca	1035		
545 Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser			
W--> 546	335	340	345
548 tct tcg ctt tgg att gga aat cgg ttt tgg tct gac ata acc gat	1080		
549 Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp			
W--> 550	350	355	360
552 ttt gta att cgg cct ttt gtg ttc cag gca aat cga cac ttt gat	1125		

misaligned nos.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:36

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

553 Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp
W--> 554

365

370

375

556 ttc aac caa gag aca gca ggt tgg agc acc cca agg ttt cgc cca
557 Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro

W--> 558

380

385

390

560 att act atc act atc agt gtt aag gag tca gca aag ctt ggt att
561 Ile Thr Ile Thr Ser Val Lys Glu Ser Ala Lys Leu Gly Ile

W--> 562

395

400

405

564 gga gtg gcc acc gac tac att gtt ccc ggc ata cca gat gga tgg
565 Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp

W--> 566

410

415

420

568 ccc gac aca aca atc cca ggt gag ttg gta cct gtt ggt gac tat
569 Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr

W--> 570

425

430

435

572 gcc atc act aat ggc acc aac aat gat atc acc aca gct gcg cag
573 Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln

W--> 574

440

445

450

576 tac gat gca gcc act gag att aga aac aac acc aat ttc aga ggc
577 Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly

W--> 578

455

460

465

580 atg tac att tgt ggt tct ctt caa aga gct tgg ggg gat aag aag
581 Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys

W--> 582

470

475

480

584 att tca aat act gct ttt atc aca acc ggc acg gtt gat gga gcc
585 Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala

W--> 586

485

490

495

588 aaa ttg ata ccc agt aat acc att gac caa aca aaa att gcc gta
589 Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val

W--> 590

500

505

510

592 ttc caa gac aca cat gcg aat aag cat gtc cag acc tcg gac gac
593 Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp

W--> 594

515

520

525

596 aca ttg gcc ctg ctt ggt tat act ggt att ggt gag gaa gca att
597 Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile

W--> 598

530

535

540

600 ggt gct gac cgc gat aga gtt gtg cga att agc gtc ctc ccg gaa
601 Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu

W--> 602

545

550

555

604 cgt ggc gca cgt ggt ggc aat cac cca atc ttc cac aaa aac tct
605 Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser

W--> 606

residual nos.

	560	565	570
608 atc aag ctt ggt tat gta att agg tcc att gat gtg ttc aat tct		1755	
609 Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser			
W--> 610	575	580	585
612 caa att ctg cat acc tct agg caa ctt tcc ctc aat cat tac tta		1800	
613 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu			
W--> 614	590	595	600
616 ttg tcg cct gac tcc ttt gct gtc tat agg att att gac tct aat		1845	
617 Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn			

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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

688 <211> LENGTH: 40
690 <212> TYPE: DNA
692 <213> ORGANISM: artificial sequence
W--> 694 <220> FEATURE: primer P3
696 <223> OTHER INFORMATION:
E--> 698 <400> SEQUENCE: ①/0<
699 gatacctatc acggagaaat tagatcctga tagaatcg 40
702 <210> SEQ ID NO: 11
704 <211> LENGTH: 22
706 <212> TYPE: DNA
708 <213> ORGANISM: artificial sequence
W--> 710 <220> FEATURE: primer P1
712 <223> OTHER INFORMATION:
E--> 714 <400> SEQUENCE: ①/1<
715 attaaacgca aatatccatg gg 22
718 <210> SEQ ID NO: 12
720 <211> LENGTH: 27
722 <212> TYPE: DNA
724 <213> ORGANISM: artificial sequence
W--> 726 <220> FEATURE: primer F2
728 <223> OTHER INFORMATION:
E--> 730 <400> SEQUENCE: ①/2<
731 gcggtaccct ggggttaggc gatagag 27
734 <210> SEQ ID NO: 13
736 <211> LENGTH: 20
738 <212> TYPE: DNA
740 <213> ORGANISM: artificial sequence
W--> 742 <220> FEATURE: primer P5
744 <223> OTHER INFORMATION:
E--> 746 <400> SEQUENCE: ①/3<
747 atttctccgt gataggtatc 20
750 <210> SEQ ID NO: 14
752 <211> LENGTH: 22
754 <212> TYPE: DNA
756 <213> ORGANISM: artificial sequence
W--> 758 <220> FEATURE: primer P5
760 <223> OTHER INFORMATION:
E--> 762 <400> SEQUENCE: ①/4<
763 ggcctctctg ttaacgtaat gg 22
766 <210> SEQ ID NO: 15
768 <211> LENGTH: 22
770 <212> TYPE: DNA
772 <213> ORGANISM: artificial sequence
W--> 774 <220> FEATURE: primer P2
776 <223> OTHER INFORMATION:
E--> 778 <400> SEQUENCE: ①/5<
779 gcgtcgaagt ttgagcatgt gc 22
782 <210> SEQ ID NO: 16
784 <211> LENGTH: 40

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
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786 <212> TYPE: DNA
788 <213> ORGANISM: artificial sequence
W--> 790 <220> FEATURE: primer P4
792 <223> OTHER INFORMATION:
E--> 794 <400> SEQUENCE: ①/6
795 ctctagcgcc taacccagg cgaccgacga caacccttat 40
799 <210> SEQ ID NO: 17
801 <211> LENGTH: 840
803 <212> TYPE: DNA
805 <213> ORGANISM: feline infectious peritonitis virus
807 <220> FEATURE:
809 <223> OTHER INFORMATION:
E--> 811 <400> SEQUENCE: ①/7
812 aaaccaaggc atataatccc gacgaaggcat ttttggttg aactaaacaa a 51
814 atg aag tac att ttg cta ata ctc gcg tgc ata att gca tgc gtt 96
815 Met Lys Tyr Ile Leu Leu Ile Leu Ala Cys Ile Ile Ala Cys Val
W--> 816
818 tat ggt gaa cgc tac tgt gcc atg caa gac agt ggc ttg cag tgt 141
819 Tyr Gly Glu Arg Tyr Cys Ala Met Gln Asp Ser Gly Leu Gln Cys
W--> 820
822 att aat ggc aca aat tca aga tgt caa acc tgc ttt gaa cgt ggt 186
823 Ile Gln Gly Thr Gln Ser Arg Cys Gln Thr Cys Phe Glu Arg Gly
W--> 824
826 gat ctt att tgg cat ctt gct aac tgg aac ttc agc tgg tct gta 231
827 Asp Leu Ile Trp His Leu Ala Asn Trp Asn Phe Ser Trp Ser Val
W--> 828
830 ata ttg att gtt ttt ata aca gtg tta caa tat ggc aga cca caa 276
831 Ile Leu Ile Val Phe Ile Thr Val Leu Gln Tyr Gly Arg Pro Gln
W--> 832
834 ttt agc tgg ctc gtt tat ggc att aaa atg ctg atc atg tgg cta 321
835 Phe Ser Trp Leu Val Tyr Gly Ile Lys Met Leu Ile Met Trp Leu
W--> 836
838 tta tgg cct att gtt cta gcg ctt acg att ttt aat gca tac tct 366
839 Leu Trp Pro Ile Val Leu Ala Leu Thr Ile Phe Asn Ala Tyr Ser
W--> 840
842 gag tac caa gtt tcc aga tat gta atg ttc ggc ttt agt gtt gca 411
843 Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala
W--> 844
846 ggt gca gtt gta acg ttt gca ctt tgg atg atg tat ttt gtg aga 456
847 Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg
W--> 848
850 tct gtt cag cta tat aga aga acc aaa tca tgg tgg tct ttt aat 501
W--> 851 Ser Val Gln Leu Tyr Arg Arg Thr Lys Ser Trp Trp Ser Phe Asn
W--> 852

*misaligned
overlaid
nos.*

	140	145
854 cct gag act aat gca att ctt tgt gtt aat gca ttg ggt aga agt	546	
855 Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser		
W--> 856		
	155	160
858 tat gtg ctt ccc tta gat ggt act cct aca ggt gtt acc ctt act	591	
859 Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr		

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
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*mesolyzed amino
hos*

W--> 860

170 175
636

862 cta ctt tca gga aat cta tat gct gaa ggt ttc aaa atg gct ggt
863 Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly

W--> 864

185 190
681

866 ggt tta acc atc gag cat ttg cct aaa tac gtc atg att gct aca
867 Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr

W--> 868

200 205
726

870 cct agt aga acc atc gtt tat aca tta gtt gga aaa caa tta aaa
871 Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys

W--> 872

215 220
771

874 gca act act gcc aca gga tgg gct tac tac gta aaa tct aaa gct
875 Ala Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala

W--> 876

230 235
816

878 ggt gat tac tca aca gaa gca cgt act gac aat ttg agt gaa cat
879 Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His

W--> 880

245 250

882 gaa aaa tta tta cat atg gtg taa 840
883 Glu Lys Leu Leu His Met Val

884 260

886 <210> SEQ ID NO: 18

888 <211> LENGTH: 1144

890 <212> TYPE: DNA

892 <213> ORGANISM: feline infectious peritonitis virus

894 <220> FEATURE:

896 <223> OTHER INFORMATION:

E--> 898 <400> SEQUENCE: ①186

899 atg gcc aca cag gga caa cgc gtc aac tgg gga gat gaa cct tcc 45
900 Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser

W--> 901

1 5 10

903 aaa aga cgt ggt cgt tct aac tct cgt ggt cgg aag aat aat gat
904 Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp

W--> 905

20 25

907 ata cct ttg tca ttc tac aac ccc att acc ctc gaa caa gga tct
908 Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser

W--> 909

35 40

911 aaa ttt tgg aat tta tgt ccg aga gac ctt gtt ccc aaa gga ata
912 Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile

W--> 913

50 55

915 ggt aat aag gat caa caa att ggt tat tgg aat aga cag att cgt
916 Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg

W--> 917

65 70

919 tat cgt att gta aaa ggc cag cgt aag gaa ctc gct gag agg tgg

920 Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp
W--> 921

Mesalipid 105

80

85

315

923 ttc ttt tac ttc tta ggt aca gga cct cat gct gat gct aaa ttc
924 Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
W--> 925

95

100

360

927 aaa gac aag att gat gga gtc ttc tgg gtt gca agg gat ggt gcc
928 Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala

RAW SEQUENCE LISTING
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*resubm'd
no 3.*

W--> 929

110
405

115

931 atg aac aag ccc aca acg ctt ggc act cgt gga acc aat aac gaa
932 Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu

W--> 933

125
450

130

935 tcc aaa cca ctg aga ttt gat ggt aag ata ccg cca cag ttt cag
936 Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln

W--> 937

140
495

145

939 ctt gaa gtg aac cgt tct agg aac aat tca agg tct ggt tct cag
940 Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln

W--> 941

155
540

160

943 tct aga tct gtt tca aga aac aga tct caa tct aga gga aga cac
944 Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His

W--> 945

170
585

175

947 cat tcc aat aac cag aat aat gtt gag gat aca att gta gcc
948 His Ser Asn Asn Gln Asn Asn Val Glu Asp Thr Ile Val Ala

W--> 949

185
630

190

951 gtg ctt gaa aaa tta ggt gtt act gac aaa caa agg tca cgt tct
952 Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser

W--> 953

200
675

205

955 aaa cct aga gaa cgt agt gat tcc aaa cct agg gac aca aca cct
956 Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro

W--> 957

215
720

220

959 aag aat gcc aac aaa cac acc tgg aag aaa act gca ggc aag gga
960 Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly

W--> 961

230
765

235

963 gat gtg aca act ttc tat ggt gct aga agt agt tca gct aac ttt
964 Asp Val Thr Thr Phe Tyr Ala Arg Ser Ser Ser Ala Asn Phe

W--> 965

245
810

250

967 ggt gat agt gat ctc gtt gcc aat ggt aac gct gcc aaa tgc tac
968 Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Lys Cys Tyr

W--> 969

260
855

265

971 cct cag ata gct gaa tgt gtt cca tca gtg tct agc ata atc ttt
972 Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe

W--> 973

275
900

280

975 ggc agt caa tgg tct gct gaa gaa gct ggt gat caa gtg aaa gtc
976 Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val

W--> 977

290
945

295

979 acg ctc act cac acc tac tac ctg cca aag gat gat gcc aaa act
980 Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr

W--> 981

presaged

983	agt caa ttc cta gaa cag att gac gct tac aag cga cct tct gaa	305	310
W--> 984	Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys Atg Pro Ser Glu	990	
W--> 985			
987	gtg gct aag gat cag agg caa aga aga tcc cgt tct aag tct gct	320	325
988	Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala	1035	
W--> 989			
991	gat aag aag cct gag gag ttg tct gta act ctt gtg gag gca tac	335	340
992	Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr	1080	
W--> 993			
		350	355
			360

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Input Set : A:\Sequence Listing - Scott et al
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995 aca gat gtg ttt gat gac aca cag gtt gag atg att gat gag gtt 1125
996 Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val

W--> 997

365

370

375

999 acg aac taa acgcattgtc 1144

1000 Thr Asn

1001 377

1004 <210> SEQ ID NO: 19

1006 <211> LENGTH: 1979 1980

1008 <212> TYPE: DNA

1010 <213> ORGANISM: feline leukemia virus

1012 <220> FEATURE:

1014 <223> OTHER INFORMATION:

E--> 1016 <400> SEQUENCE: ① 19 ←

E--> 1017 accaccaatc aagacatcttc ggacagcccc agctcgtggacg atccatcaag

E--> 1019 atg gaa agt cca acg ccc cca aaa ccc tct aaa gat aag act ctc
1020 Met Glu Ser Pro Thr His Pro Ser Lys Pro Asp Lys Thr Leu

W--> 1021

misaligned amino 1 5 10
E--> 1023 tcg tgg aac tta gcg ttt ctg gtg ggg atc tta ttt aca ata gac
1024 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp

W--> 1025

E--> 1027 ata gga atg gcc aat cct agt cca cac caa ata tat aat gta act
1028 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr

W--> 1029

E--> 1031 tgg gta ata acc aat gta caa act aac acc caa gct aac gcc acc
1032 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr

1033 50 55 60

E--> 1035 tct atg tta gga acc tta acc gat gcc tac cct acc cta cat gtt
1036 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val

1037 65 70 75

E--> 1039 gac tta tgt gac cta gtg gga gac acc tgg gaa cct ata gtc cta
1040 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

1041 80 85 90

E--> 1043 aac cca acc aat gta aaa cac ggg gca cgt tac tcc tcc tca aaa
1044 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys

W--> 1045 95 100 105

E--> 1047 tat gga tgt aaa act aca gat aga aaa aaa cag caa cag aca tac
1048 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr

W--> 1049 110 115 120

E--> 1051 ccc ttt tac gtc tgc ccc gga cat gcc ccc tgg tgg ggg cca aag
1052 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys

W--> 1053 125 130 135

E--> 1055 gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg
1056 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp

W--> 1057 140 145 150

E--> 1059 gga tgt gag acc acc gga gaa gct tgg tgg aag ccc acc tcc tca
1060 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser

W--> 1061 155 160 165

E--> 1063 tgg gac tat atc aca gta aaa aga ggg agt agt cag gac aat agc
1064 Trp Asp Tyr Ile Val Lys Arg Gly Ser Ser Gln Asp Asn Ser

RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al
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W--> 1065	170	175	180	
E--> 1067	tgt gag gga aaa tgc aac ccc ctg gtt ttg cag ttc acc cag aag			635
1068	Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys			
W--> 1069	185	190	195	
E--> 1072	gga aga caa gcc tct tgg gac gga cct aag atg tgg gga ttg cga			680
1073	Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg			
W--> 1074	200	205	210	
E--> 1076	cta tac cgt aca gga tat gac cct atc gct tta ttc acg gtg tcc			725
1077	Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser			
W--> 1078				
			215	220
E--> 1080	cggt cag gta tca acc att acg ccg cct cag gca atg gga cca aac			770
1081	Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn			
W--> 1082	230	235	240	
E--> 1084	cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca			815
1085	Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr			
W--> 1086	245	250	255	
E--> 1088	ggg tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc			860
1089	Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala			
W--> 1090	260	265	270	
E--> 1092	cca agg tct gtt gcc ccc acc acc atg ggt ccc aaa cgg att ggg			905
1093	Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly			
W--> 1094	275	280	285	
E--> 1096	acc gga gat agg tta ata aat tta gta caa ggg aca tac cta gcc			950
1097	Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala			
W--> 1098	290	295	300	
E--> 1100	tta aat gcc acc gac ccc aac aaa act aaa gac tgt tgg ctc tgc			995
1101	Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys			
W--> 1102	305	310	315	
E--> 1104	ctg gtt tct cga cca ccc tat tac gaa ggg att gca atc tta ggt			1040
1105	Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly			
W--> 1106	320	325	330	
E--> 1108	acc tac agc aac caa aca aac ccc cca tcc tgc cta tct act			1085
1109	Asn Tyr Ser Asn Gln Thr Asn Pro Pro Ser Cys Leu Ser Ile			
W--> 1110	335	340	345	
E--> 1114	ccg caa cac aaa cta act ata tct gaa gta tca ggg caa gga atg			1130
1115	Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met			
W--> 1116	350	355	360	
E--> 1118	tgc ata ggg act gtt cct aaa acc cac cag gct ttg tgc aat aag			1175
1119	Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys			
W--> 1120	365	370	375	
E--> 1122	aca caa cag gga cat aca ggg gcg cac tat cta gcc gcc ccc aac			1220
1123	Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn			
W--> 1124	380	385	390	
E--> 1126	ggc acc tat tgg gcc tgc aac act gga ctc acc cca tgc att tcc			1265
1127	Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser			
W--> 1128	395	400	405	
E--> 1130	atg gcg gtg ctc aat tgg acc tct gat ttt tgt gtc tta atc gaa			1310
1131	Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu			
W--> 1132	410	415	420	

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Input Set : A:\Sequence Listing - Scott et al
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E--> 1134 tta tgg ccc aga gtg act tac cat caa ccc gaa tat gtg tac aca	1355
1135 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr	
W--> 1136 425 430 435	1400
E--> 1138 cat ttt gcc aaa gct gtc agg ttc cga aga gaa cca ata tca cta	
W--> 1139 His Phe Ala Lys Ala Val Arg Phe Arg Axa Glu Pro Ile Ser Leu	
W--> 1140 440 445 450	1445
E--> 1142 acg gtt gcc ctt atg ttg gga gga ctt act gta ggg ggc ata gcc	
1143 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala	
W--> 1144 455 460 465	1490
E--> 1146 gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag	
1147 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln	
W--> 1148 470 475 480	1535
E--> 1151 ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta	
1152 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu	
W--> 1153 485 490 495	1580
E--> 1156 gaa gaa tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct	
1157 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser	
W--> 1158 500 505 510	1625
E--> 1160 gaa gta gtc tta caa aac aga cgg ggc cta gat att cta ttc tta	
1161 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu	
W--> 1162 515 520 525	1670
E--> 1164 caa gag gga ggg ctc tgt gcc gca ttg aaa gaa gaa tgt tgc ttc	
1165 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe	
W--> 1166 530 535 540	1715
E--> 1168 tat gcg gat cac acc gga ctc gtc cga gac aat atg gcc aaa tta	
1169 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu	
W--> 1170 545 550 555	1760
E--> 1172 aga gaa aga cta aaa cag cgg caa caa ctg ttt gac tcc caa cag	
1173 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln	
W--> 1174 560 565 570	1805
E--> 1176 gga tgg ttt gaa gga tgg ttc aac aag tcc ccc tgg ttt aca acc	
1177 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr	
W--> 1178 575 580 585	1850
E--> 1180 cta att tcc tcc att atg ggc ccc tta cta atc cta ctc cta att	
1181 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Ile	
W--> 1182 590 595 600	
E--> 1184 ctc ctc ttc ggc cca tgc atc ctt aac cga tta gta caa ttc gta	
W--> 1185 1895 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe	
W--> 1186 Val	
W--> 1187 605 610 615	
E--> 1189 aaa gac aga ata tct gtg gta cag gct tta att tta acc caa cag	
W--> 1190 1940 Lys Asp Axa Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln	
W--> 1191 Gln	
W--> 1192 620 625 630	1979
E--> 1194 tac caa cag ata aag caa tac gat ccg gac cga cca tga	
1195 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro	
E--> 1196 635 640	
1199 <210> SEQ ID NO: 20	
1201 <211> LENGTH: 584	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:37

Input Set : A:\Sequence Listing - Scott et al
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1203 <212> TYPE: PRT
1205 <213> ORGANISM: feline panleukopenia peritonitis virus
1207 <220> FEATURE:
1209 <223> OTHER INFORMATION:
E--> 1211 <400> SEQUENCE: 120 *mesaligned
answ and
nos.*
1212 Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val
E--> 1213

1215 Arg Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly
E--> 1216 20 25 30
1218 Gly Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe
E--> 1219 35 40 45
1221 Asn Asn Gln Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu
E--> 1222 50 55 60
1224 Ile Thr Ala Asn Ser Ser Arg Leu Val His Leu Asn Met Pro Glu
E--> 1225 65 70 75
1227 Ser Glu Asn Tyr Lys Arg Val Val Val Asn Asn Met Asp Lys Thr
E--> 1228 80 85 90
1230 Ala Val Lys Gly Asn Met Ala Leu Asp Asp Thr His Val Gln Ile
E--> 1231 95 100 105
1233 Val Thr Pro Trp Ser Leu Val Asp Ala Asn Ala Trp Gly Val Trp
E--> 1234 110 115 120
1236 Phe Asn Pro Gly Asp Trp Gln Leu Ile Val Asn Thr Met Ser Glu
E--> 1237 125 130 135
1239 Leu His Leu Val Ser Phe Glu Gln Glu Ile Phe Asn Val Val Leu
E--> 1240 140 145 150
1242 Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro Thr Lys Val Tyr
E--> 1243 155 160 165
1245 Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu Asp Ser Asn
E--> 1246 170 175 180
1248 Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu Thr Leu
E--> 1249 185 190 195
1251 Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg Tyr
E--> 1252 200 205 210
1255 Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
E--> 1256 215 220 225
1258 Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp
E--> 1259 230 235 240
1261 Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu
E--> 1262 245 250 255
1264 Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Asp Cys
E--> 1265 260 265 270 *invac*
E--> 1268 Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn Asp Ala Leu
E--> 1269 275 280 285
1271 Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala
E--> 1272 290 295 300
1274 Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly
E--> 1275 305 310 315
1277 Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile
E--> 1278 320 325 330

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1280	Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe			
E--> 1281	335	340	345	
1283	Glu Ala Ser Thr Gln Gly Pro Phe Lys Ile Pro Ile Ala Ala Gly			
E--> 1284	350	355	360	
1286	Arg Gly Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp			
E--> 1287	365	370	375	
1289	Pro Arg Tyr Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr			
E--> 1290	380	385	390	
1292	Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp			
E--> 1293	395	400	405	
1295	Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn Ile Asn Phe			
E--> 1296	410	415	420	
1298	Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr Asp Pro			
E--> 1299	425	430	435	
1302	Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn Thr			
E--> 1303	440	445	450	
1305	Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro			
E--> 1306	455	460	465	
1309	Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro			
E--> 1310	470	475	480	
1312	Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro			
E--> 1313	485	490	495	
1315	Gly Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr			
E--> 1316	500	505		510
1319	Asp Pro Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser			
E--> 1320	515	520	525	
1322	Asp Phe Trp Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg			
E--> 1323	530	535	540	
1325	Ala Ser His Thr Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val			
E--> 1326	545	550	555	
1328	Asp Asn Gln Phe Asn Tyr Leu Pro Asn Asn Ile Gly Ala Met Lys			
E--> 1329	560	565	570	
1332	Ile Val Tyr Glu Lys Ser Gln Leu Ala Pro Arg Lys Leu Tyr			
E--> 1333		575		580
1336	<210> SEQ ID NO: 21			
1338	<211> LENGTH: 524			
1340	<212> TYPE: PRT			
1342	<213> ORGANISM: rabies virus			
1344	<220> FEATURE:			
1346	<223> OTHER INFORMATION:			
E--> 1348	<400> SEQUENCE: ① 21			
1349	Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe			
E--> 1350	1	5		10
1352	Pro Leu Cys Phe Gly Lys Phe Pro Ile Tyr Thr Ile Leu Asp			
E--> 1353	15	20		25
1355	Lys Leu Gly Pro Trp Ser Pro Ile Asp Ile His His Leu Ser			
E--> 1356	30	35		40
1358	Cys Pro Asn Asn Leu Val Val Glu Asp Glu Gly Cys Thr Asn			
E--> 1359	45		50	5

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
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1362 Leu Ser Gly Phe Ser Tyr Met Glu Leu Lys Val Gly Tyr Ile
E--> 1363 60 65

1365 Leu Ala Ile Lys Met Asn Gly Phe Thr Cys Thr Gly Val Val
E--> 1366 75 80

1368 Thr Glu Ala Glu Thr Tyr Thr Asn Phe Val Gly Tyr Val Thr
E--> 1369 85 90 95

1371 Thr Thr Phe Lys Arg Lys His Phe Arg Pro Thr Pro Asp Ala
E--> 1372 100 105 110

1374 Cys Arg Ala Ala Tyr Asn Trp Lys Met Ala Gly Asp Pro Arg
E--> 1375 115 120 125

1377 Tyr Glu Glu Ser Leu His Asn Pro Tyr Pro Asp Tyr Arg Trp
E--> 1378 130 135 140

1380 Leu Arg Thr Val Lys Thr Lys Glu Ser Leu Val Ile Ile
E--> 1381 145 150

1383 Ser Pro Ser Val Ala Asp Leu Asp Pro Tyr Asp Arg Ser Leu
E--> 1384 155 160 165

1386 His Ser Arg Val Phe Pro Ser Gly Lys Cys Ser Gly Val Ala
E--> 1387 170 175 180

1389 Val Ser Ser Thr Tyr Cys Ser Thr Asn His Asp Tyr Thr Ile
E--> 1390 185 190 195

1392 Trp Met Pro Glu Asn Pro Arg Leu Gly Met Ser Cys Asp Ile
E--> 1393 200 205 210

1395 Phe Thr Asn Ser Arg Gly Lys Arg Ala Ser Lys Gly Ser Glu
E--> 1396 215 220

1398 Thr Cys Gly Phe Val Asp Glu Arg Gly Leu Tyr Lys Ser Leu
E--> 1399 225 230 235

1401 Lys Gly Ala Cys Lys Leu Lys Leu Cys Gly Val Leu Gly Leu
E--> 1402 240 245 250

1404 Arg Leu Met Asp Gly Thr Trp Val Ala Met Gln Thr Ser Asn
E--> 1405 255 260 265

1407 Glu Thr Lys Trp Cys Pro Pro Asp Gln Leu Val Asn Leu His
E--> 1408 270 275 280

1411 Asp Phe Arg Ser Asp Glu Ile Glu His Leu Val Val Glu Glu
E--> 1412 *in Val* 285 290

E--> 1414 Leu Val Arg *Lsy* Arg Glu Glu Cys Leu Asp Ala Leu Glu Ser
E--> 1415 295 300 305

1417 Ile Met Thr Thr Lys Ser Val Ser Phe Arg Arg Leu Ser His
E--> 1418 310 315 320

1420 Leu Arg Lys Leu Val Pro Gly Phe Gly Lys Ala Tyr Thr Ile
E--> 1421 325 330 335

1423 Phe Asn Lys Thr Leu Met Glu Ala Asp Ala His Tyr Lys Ser
E--> 1424 340 345

1426 Val Arg Thr Trp Asn Glu Ile Leu Pro Ser Lys Gly Cys Leu
E--> 1427 355 360

1429 Arg Val Gly Gly Arg Cys His Pro His Val Asn Gly Val Phe
E--> 1430 365 370 375

1432 Phe Asn Gly Ile Ile Leu Gly Pro Asp Gly Asn Val Leu Ile
E--> 1433 380 385

1435 Pro Glu Met Gln Ser Ser Leu Leu Gln Gln His Met Glu Leu
390

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

*resigned
no 3*

E--> 1436

395

400

40

1438 Leu Glu Ser Ser Val Ile Pro Leu Val His Pro Leu Ala Asp

E--> 1439

410

415

1441 Pro Ser Thr Val Phe Lys Asp Gly Asp Glu Ala Glu Asp Phe

E--> 1442

425

430

1444 Val Glu Val His Leu Pro Asp Val His Asn Gln Val Ser Gly

E--> 1445

435

440

445

1447 Val Asp Leu Gly Leu Pro Asn Trp Gly Lys Tyr Val Leu Leu

E--> 1448

450

455

460

1450 Ser Ala Gly Ala Leu Thr Ala Leu Met Leu Ile Ile Phe Leu

E--> 1451

465

470

47

1453 Met Thr Cys Cys Arg Arg Val Asn Arg Ser Glu Pro Thr Gln

E--> 1454

480

485

1456 His Asn Leu Arg Gly Thr Gly Arg Glu Val Ser Val Thr Pro

E--> 1457

495

500

1459 Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser His Lys Ser

E--> 1460

505

510

515

1463 Gly Gly Glu Thr Arg Leu

E--> 1464

520

524

1467 <210> SEQ ID NO: 22

1469 <211> LENGTH: 668

1471 <212> TYPE: PRT

1473 <213> ORGANISM: feline calicivirus

1475 <220> FEATURE:

1477 <223> OTHER INFORMATION:

E--> 1479 <400> SEQUENCE: ① 22

1480 Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp

E--> 1481

1

5

10

1483 Pro His Ile Lys Leu Val Ile Asn Pro Asn Lys Phe Leu His Val

E--> 1484

20

25

1486 Gly Phe Cys Asp Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu

E--> 1487

35

40

1489 Pro Glu Phe Gly Thr Met Trp Asp Cys Asp Gln Ser Pro Leu Gln

E--> 1490

50

55

1492 Val Tyr Leu Glu Ser Ile Leu Gly Asp Asp Glu Trp Ser Ser Thr

E--> 1493

65

70

1495 His Glu Ala Ile Asp Pro Val Val Pro Pro Met His Trp Asp Glu

E--> 1496

80

85

1498 Ala Gly Lys Ile Phe Gln Pro His Pro Gly Val Leu Met His His

E--> 1499

95

100

1501 Leu Ile Cys Lys Val Ala Glu Gly Trp Asp Pro Asn Leu Pro Leu

E--> 1502

1504 Phe Arg Leu Glu Ala Asp Asp Gly Ser Ile Thr Thr Pro Glu Gln

E--> 1505

110

115

125

130

1507 Gly Thr Met Val Gly Gly Val Ile Ala Glu Pro Asn Ala Gln Met

E--> 1508

140

145

1510 Ser Thr Ala Ala Asp Met Ala Thr Gly Lys Ser Val Asp Ser Glu

E--> 1511

155

160

1513 Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val Asn Trp Ser Thr

residues 109

RAW SEQUENCE LISTING

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DATE: 06/21/2001

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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw*me signed
no*

E--> 1514	170	175
1516 Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser Leu Gly Pro		
E--> 1517	185	190
1519 Leu Leu Asn Pro Tyr Leu Thr His Leu Ala Lys Leu Tyr Val Ala		
E--> 1520	200	205
1522 Trp Ser Gly Ser Val Asp Val Arg Phe Ser Ile Ser Gly Ser Gly		
E--> 1523	215	220
1525 Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Ile		
E--> 1526	230	235
1528 Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu		
E--> 1529	245	250
1531 Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Ser Ile Pro Asp		
E--> 1532	260	265
1534 Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr		
E--> 1535	275	280
1537 Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala		
E--> 1538	290	295
1540 Asn Asp Ser Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys		
E--> 1541	305	310
1543 Pro Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser		
E--> 1544	320	325
1546 Met Leu Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Ser		
E--> 1547	335	340
1549 Ser Ser Leu Trp Ile Gly Asn Arg Phe Trp Ser Asp Ile Thr Asp		
E--> 1550	350	355
1552 Phe Val Ile Arg Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp		
E--> 1553	365	370
1555 Phe Asn Gln Glu Thr Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro		
E--> 1556	380	385
1558 Ile Thr Ile Thr Ile Ser Val Lys Glu Ser Ala Lys Leu Gly Ile		
E--> 1559	395	400
1561 Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile Pro Asp Gly Trp		
E--> 1562	410	415
1564 Pro Asp Thr Thr Ile Pro Gly Glu Leu Val Pro Val Gly Asp Tyr		
E--> 1565	425	430

*misaligned
105.*

1567 Ala Ile Thr Asn Gly Thr Asn Asn Asp Ile Thr Thr Ala Ala Gln			
E--> 1568	440	445	450
1570 Tyr Asp Ala Ala Thr Glu Ile Arg Asn Asn Thr Asn Phe Arg Gly			
E--> 1571	455	460	465
1573 Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys			
E--> 1574	470	475	480
1576 Ile Ser Asn Thr Ala Phe Ile Thr Thr Gly Thr Val Asp Gly Ala			
E--> 1577	485	490	495
1579 Lys Leu Ile Pro Ser Asn Thr Ile Asp Gln Thr Lys Ile Ala Val			
E--> 1580	500	505	510
1582 Phe Gln Asp Thr His Ala Asn Lys His Val Gln Thr Ser Asp Asp			
E--> 1583	515	520	525
1585 Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Glu Ala Ile			
E--> 1586	530	535	540

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881

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Input Set : A:\Sequence Listing - Scott et al
 Output Set: N:\CRF3\06212001\I873881.raw

1588 Gly Ala Asp Arg Asp Arg Val Val Arg Ile Ser Val Leu Pro Glu
 E--> 1589 545 550 555
 1591 Arg Gly Ala Arg Gly Gly Asn His Pro Ile Phe His Lys Asn Ser
 E--> 1592 560 565 570
 1594 Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser
 E--> 1595 575 580 585
 1597 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu
 E--> 1598 590 595 600
 1600 Leu Ser Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn
 E--> 1601 605 610 615
 1603 Gly Ser Trp Phe Asp Ile Gly Ile Asp Asn Asp Gly Phe Ser Phe
 E--> 1604 620 625 630
 1606 Val Gly Val Ser Ser Ile Gly Lys Leu Glu Phe Pro Leu Thr Ala
 E--> 1607 635 640 645
 1609 Ser Tyr Met Gly Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn
 E--> 1610 650 655 660
 1612 Ile Arg Ser Val Met Thr Lys Leu
 E--> 1613 665
 1616 <210> SEQ ID NO: 23
 1618 <211> LENGTH: 262
 1620 <212> TYPE: PRT
 1622 <213> ORGANISM: feline infectious peritonitis virus
 1624 <220> FEATURE:
 1626 <223> OTHER INFORMATION:
 E--> 1628 <400> SEQUENCE: 123 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995 1000 1005 1010 1015 1020 1025 1030 1035 1040 1045 1050 1055 1060 1065 1070 1075 1080 1085 1090 1095 1100 1105 1110 1115 1120 1125 1130 1135 1140 1145 1150 1155 1160 1165 1170 1175 1180 1185 1190 1195 1200 1205 1210 1215 1220 1225 1230 1235 1240 1245 1250 1255 1260 1265 1270 1275 1280 1285 1290 1295 1300 1305 1310 1315 1320 1325 1330 1335 1340 1345 1350 1355 1360 1365 1370 1375 1380 1385 1390 1395 1400 1405 1410 1415 1420 1425 1430 1435 1440 1445 1450 1455 1460 1465 1470 1475 1480 1485 1490 1495 1500 1505 1510 1515 1520 1525 1530 1535 1540 1545 1550 1555 1560 1565 1570 1575 1580 1585 1590 1595 1600 1605 1610 1615 1620 1625 1630 1635 1640 1645 1650 1655 1660 1665 1670 1675 1680 1685 1690 1695 1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1760 1765 1770 1775 1780 1785 1790 1795 1800 1805 1810 1815 1820 1825 1830 1835 1840 1845 1850 1855 1860 1865 1870 1875 1880 1885 1890 1895 1900 1905 1910 1915 1920 1925 1930 1935 1940 1945 1950 1955 1960 1965 1970 1975 1980 1985 1990 1995 2000 2005 2010 2015 2020 2025 2030 2035 2040 2045 2050 2055 2060 2065 2070 2075 2080 2085 2090 2095 2100 2105 2110 2115 2120 2125 2130 2135 2140 2145 2150 2155 2160 2165 2170 2175 2180 2185 2190 2195 2200 2205 2210 2215 2220 2225 2230 2235 2240 2245 2250 2255 2260 2265 2270 2275 2280 2285 2290 2295 2300 2305 2310 2315 2320 2325 2330 2335 2340 2345 2350 2355 2360 2365 2370 2375 2380 2385 2390 2395 2400 2405 2410 2415 2420 2425 2430 2435 2440 2445 2450 2455 2460 2465 2470 2475 2480 2485 2490 2495 2500 2505 2510 2515 2520 2525 2530 2535 2540 2545 2550 2555 2560 2565 2570 2575 2580 2585 2590 2595 2600 2605 2610 2615 2620 2625 2630 2635 2640 2645 2650 2655 2660 2665 2670 2675 2680 2685 2690 2695 2700 2705 2710 2715 2720 2725 2730 2735 2740 2745 2750 2755 2760 2765 2770 2775 2780 2785 2790 2795 2800 2805 2810 2815 2820 2825 2830 2835 2840 2845 2850 2855 2860 2865 2870 2875 2880 2885 2890 2895 2900 2905 2910 2915 2920 2925 2930 2935 2940 2945 2950 2955 2960 2965 2970 2975 2980 2985 2990 2995 3000 3005 3010 3015 3020 3025 3030 3035 3040 3045 3050 3055 3060 3065 3070 3075 3080 3085 3090 3095 3100 3105 3110 3115 3120 3125 3130 3135 3140 3145 3150 3155 3160 3165 3170 3175 3180 3185 3190 3195 3200 3205 3210 3215 3220 3225 3230 3235 3240 3245 3250 3255 3260 3265 3270 3275 3280 3285 3290 3295 3300 3305 3310 3315 3320 3325 3330 3335 3340 3345 3350 3355 3360 3365 3370 3375 3380 3385 3390 3395 3400 3405 3410 3415 3420 3425 3430 3435 3440 3445 3450 3455 3460 3465 3470 3475 3480 3485 3490 3495 3500 3505 3510 3515 3520 3525 3530 3535 3540 3545 3550 3555 3560 3565 3570 3575 3580 3585 3590 3595 3600 3605 3610 3615 3620 3625 3630 3635 3640 3645 3650 3655 3660 3665 3670 3675 3680 3685 3690 3695 3700 3705 3710 3715 3720 3725 3730 3735 3740 3745 3750 3755 3760 3765 3770 3775 3780 3785 3790 3795 3800 3805 3810 3815 3820 3825 3830 3835 3840 3845 3850 3855 3860 3865 3870 3875 3880 3885 3890 3895 3900 3905 3910 3915 3920 3925 3930 3935 3940 3945 3950 3955 3960 3965 3970 3975 3980 3985 3990 3995 4000 4005 4010 4015 4020 4025 4030 4035 4040 4045 4050 4055 4060 4065 4070 4075 4080 4085 4090 4095 4100 4105 4110 4115 4120 4125 4130 4135 4140 4145 4150 4155 4160 4165 4170 4175 4180 4185 4190 4195 4200 4205 4210 4215 4220 4225 4230 4235 4240 4245 4250 4255 4260 4265 4270 4275 4280 4285 4290 4295 4300 4305 4310 4315 4320 4325 4330 4335 4340 4345 4350 4355 4360 4365 4370 4375 4380 4385 4390 4395 4400 4405 4410 4415 4420 4425 4430 4435 4440 4445 4450 4455 4460 4465 4470 4475 4480 4485 4490 4495 4500 4505 4510 4515 4520 4525 4530 4535 4540 4545 4550 4555 4560 4565 4570 4575 4580 4585 4590 4595 4600 4605 4610 4615 4620 4625 4630 4635 4640 4645 4650 4655 4660 4665 4670 4675 4680 4685 4690 4695 4700 4705 4710 4715 4720 4725 4730 4735 4740 4745 4750 4755 4760 4765 4770 4775 4780 4785 4790 4795 4800 4805 4810 4815 4820 4825 4830 4835 4840 4845 4850 4855 4860 4865 4870 4875 4880 4885 4890 4895 4900 4905 4910 4915 4920 4925 4930 4935 4940 4945 4950 4955 4960 4965 4970 4975 4980 4985 4990 4995 5000 5005 5010 5015 5020 5025 5030 5035 5040 5045 5050 5055 5060 5065 5070 5075 5080 5085 5090 5095 5100 5105 5110 5115 5120 5125 5130 5135 5140 5145 5150 5155 5160 5165 5170 5175 5180 5185 5190 5195 5200 5205 5210 5215 5220 5225 5230 5235 5240 5245 5250 5255 5260 5265 5270 5275 5280 5285 5290 5295 5300 5305 5310 5315 5320 5325 5330 5335 5340 5345 5350 5355 5360 5365 5370 5375 5380 5385 5390 5395 5400 5405 5410 5415 5420 5425 5430 5435 5440 5445 5450 5455 5460 5465 5470 5475 5480 5485 5490 5495 5500 5505 5510 5515 5520 5525 5530 5535 5540 5545 5550 5555 5560 5565 5570 5575 5580 5585 5590 5595 5600 5605 5610 5615 5620 5625 5630 5635 5640 5645 5650 5655 5660 5665 5670 5675 5680 5685 5690 5695 5700 5705 5710 5715 5720 5725 5730 5735 5740 5745 5750 5755 5760 5765 5770 5775 5780 5785 5790 5795 5800 5805 5810 5815 5820 5825 5830 5835 5840 5845 5850 5855 5860 5865 5870 5875 5880 5885 5890 5895 5900 5905 5910 5915 5920 5925 5930 5935 5940 5945 5950 5955 5960 5965 5970 5975 5980 5985 5990 5995 6000 6005 6010 6015 6020 6025 6030 6035 6040 6045 6050 6055 6060 6065 6070 6075 6080 6085 6090 6095 6100 6105 6110 6115 6120 6125 6130 6135 6140 6145 6150 6155 6160 6165 6170 6175 6180 6185 6190 6195 6200 6205 6210 6215 6220 6225 6230 6235 6240 6245 6250 6255 6260 6265 6270 6275 6280 6285 6290 6295 6300 6305 6310 6315 6320 6325 6330 6335 6340 6345 6350 6355 6360 6365 6370 6375 6380 6385 6390 6395 6400 6405 6410 6415 6420 6425 6430 6435 6440 6445 6450 6455 6460 6465 6470 6475 6480 6485 6490 6495 6500 6505 6510 6515 6520 6525 6530 6535 6540 6545 6550 6555 6560 6565 6570 6575 6580 6585 6590 6595 6600 6605 6610 6615 6620 6625 6630 6635 6640 6645 6650 6655 6660 6665 6670 6675 6680 6685 6690 6695 6700 6705 6710 6715 6720 6725 6730 6735 6740 6745 6750 6755 6760 6765 6770 6775 6780 6785 6790 6795 6800 6805 6810 6815 6820 6825 6830 6835 6840 6845 6850 6855 6860 6865 6870 6875 6880 6885 6890 6895 6900 6905 6910 6915 6920 6925 6930 6935 6940 6945 6950 6955 6960 6965 6970 6975 6980 6985 6990 6995 7000 7005 7010 7015 7020 7025 7030 7035 7040 7045 7050 7055 7060 7065 7070 7075 7080 7085 7090 7095 7100 7105 7110 7115 7120 7125 7130 7135 7140 7145 7150 7155 7160 7165 7170 7175 7180 7185 7190 7195 7200 7205 7210 7215 7220 7225 7230 7235 7240 7245 7250 7255 7260 7265 7270 7275 7280 7285 7290 7295 7300 7305 7310 7315 7320 7325 7330 7335 7340 7345 7350 7355 7360 7365 7370 7375 7380 7385 7390 7395 7400 7405 7410 7415 7420 7425 7430 7435 7440 7445 7450 7455 7460 7465 7470 7475 7480 7485 7490 7495 7500 7505 7510 7515 7520 7525 7530 7535 7540 7545 7550 7555 7560 7565 7570 7575 7580 7585 7590 7595 7600 7605 7610 7615 7620 7625 7630 7635 7640 7645 7650 7655 7660 7665 7670 7675 7680 7685 7690 7695 7700 7705 7710 7715 7720 7725 7730 7735 7740 7745 7750 7755 7760 7765 7770 7775 7780 7785 7790 7795 7800 7805 7810 7815 7820 7825 7830 7835 7840 7845 7850 7855 7860 7865 7870 7875 7880 7885 7890 7895 7900 7905 7910 7915 7920 7925 7930 7935 7940 7945 7950 7955 7960 7965 7970 7975 7980 7985 7990 7995 8000 8005 8010 8015 8020 8025 8030 8035 8040 8045 8050 8055 8060 8065 8070 8075 8080 8085 8090 8095 8100 8105 8110 8115 8120 8125 8130 8135 8140 8145 8150 8155 8160 8165 8170 8175 8180 8185 8190 8195 8200 8205 8210 8215 8220 8225 8230 8235 8240 8245 8250 8255 8260 8265 8270 8275 8280 8285 8290 8295 8300 8305 8310 8315 8320 8325 8330 8335 8340 8345 8350 8355 8360 8365 8370 8375 8380 8385 8390 8395 8400 8405 8410 8415 8420 8425 8430 8435 8440 8445 8450 8455 8460 8465 8470 8475 8480 8485 8490 8495 8500 8505 8510 8515 8520 8525 8530 8535 8540 8545 8550 8555 8560 8565 8570 8575 8580 8585 8590 8595 8600 8605 8610 8615 8620 8625 8630 8635 8640 8645 8650 8655 8660 8665 8670 8675 8680 8685 8690 8695 8700 8705 8710 8715 8720 8725 8730 8735 8740 8745 8750 8755 8760 8765 8770 8775 8780 8785 8790 8795 8800 8805 8810 8815 8820 8825 8830 8835 8840 8845 8850 8855 8860 8865 8870 8875 8880 8885 8890 8895 8900 8905 8910 8915 8920 8925 8930 8935 8940 8945 8950 8955 8960 8965 8970 8975 8980 8985 8990 8995 9000 9005 9010 9015 9020 9025 9030 9035 9040 9045 9050 9055 9060 9065 9070 9075 9080 9085 9090 9095 9100 9105 9110 9115 9120 9125 9130 9135 9140 9145 9150 9155 9160 9165 9170 9175 9180 9185 9190 9195 9200 9205 9210 9215 9220 9225 9230 9235 9240 9245 9250 9255 9260 9265 9270 9275 9280 9285 9290 9295 9300 9305 9310 9315 9320 9325 9330 9335 9340 9345 9350 9355 9360 9365 9370 9375 9380 9385 9390 9395 9400 9405 9410 9415 9420 9425 9430 9435 9440 9445 9450 9455 9460 9465 9470 9475 9480 9485 9490 9495 9500 9505 9510 9515 9520 9525 9530 9535 9540 9545 9550 9555 9560 9565 9570 9575 9580 9585 9590 9595 9600 9605 9610 9615 9620 9625 9630 9635 9640 9645 9650 9655 9660 9665 9670 9675 9680 9685 9690 9695 9700 9705 9710 9715 9720 9725 9730 9735 9740 9745 9750 9755 9760 9765 9770 9775 9780 9785 9790 9795 9800 9805 9810 9815 9820 9825 9830 9835 9840 9845 9850 9855 9860 9865 9870 9875 9880 9885 9890 9895 9900 9905 9910 9915 9920 9925 9930 9935 9940 9945 9950 9955 9960 9965 9970 9975 9980 9985 9990 9995 10000 10005 10010 10015 10020 10025 10030 10035 10040 10045 10050 10055 10060 10065 10070 10075 10080 10085 10090 10095 10100 10105 10110 10115 10120 10125 10130 10135 10140 10145 10150 10155 10160 10165 10170 10175 10180 10185 10190 10195 10200 10205 10210 10215 10220 10225 10230 10235 10240 10245 10250 10255 10260 10265 10270 10275 10280 10285 10290 10295 10300 10305 10310 10315 10320 10325 10330 10335 10340 10345 10350 10355 10360 10365 10370 10375 10380 10385 10390 10395 10400 10405 10410 10415 10420 10425 10430 10435 10440 10445 10450 10455 10460 10465 10470 10475 10480 10485 10490 10495 10500 10505 10510 10515 10520 10525 10530 10535 10540 10545 10550 10555 10560 10565 10570 10575 10580 10585 10590 10595 10600 10605 10610 10615 10620 10625 10630 10635 10640 10645 10650 10655 10660 10665 10670 10675 10680 10685 10690 10695 10700 10705 10710 10715 10720 10725 10730 10735 10740 10745 10750 10755 10760 10765 10770 10775 10780 10785 10790 10795 10800 10805 10810 10815 10820 10825 10830 10835 10840 10845 10850 10855 10860 10865 10870 10875 10880 10885 10890 10895 10900 10905 10910 10915 10920 10925 10930 10935 10940 10945 10950 10955 10960 10965 10970 10975 10980 10985 10990 10

	95	100
1650 Glu Tyr Gln Val Ser Arg Tyr Val Met Phe Gly Phe Ser Val Ala		
E--> 1651	110	115
1653 Gly Ala Val Val Thr Phe Ala Leu Trp Met Met Tyr Phe Val Arg		
E--> 1654	125	130
E--> 1656 Ser Val Gln Leu Tyr Arg Axg <i>invalid</i> Thr Lys Ser Trp Trp Ser Phe Asn		
E--> 1657	140	145
1659 Pro Glu Thr Asn Ala Ile Leu Cys Val Asn Ala Leu Gly Arg Ser		
E--> 1660	155	160
1662 Tyr Val Leu Pro Leu Asp Gly Thr Pro Thr Gly Val Thr Leu Thr		
E--> 1663	170	175

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/873,881

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TIME: 17:28:37

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

1665 Leu Leu Ser Gly Asn Leu Tyr Ala Glu Gly Phe Lys Met Ala Gly
 E--> 1666 185 190 *Resigned
WS*

1668 Gly Leu Thr Ile Glu His Leu Pro Lys Tyr Val Met Ile Ala Thr
 E--> 1669 200 205

1671 Pro Ser Arg Thr Ile Val Tyr Thr Ile Val Gly Lys Gln Leu Lys
 E--> 1672 215 220

1674 Ala Thr Thr Ala Thr Gly Trp Ala Tyr Tyr Val Lys Ser Lys Ala
 E--> 1675 230 235

1677 Gly Asp Tyr Ser Thr Glu Ala Arg Thr Asp Asn Leu Ser Glu His
 E--> 1678 245 250

1680 Glu Lys Leu Leu His Met Val
 1681 260

1684 <210> SEQ ID NO: 24

1686 <211> LENGTH: 377

1688 <212> TYPE: PRT

1690 <213> ORGANISM: feline infectious peritonitis virus

1692 <220> FEATURE:

1694 <223> OTHER INFORMATION:

E--> 1696 <400> SEQUENCE: ①74

1697 Met Ala Thr Gln Gly Gln Arg Val Asn Trp Gly Asp Glu Pro Ser
 E--> 1698 1 5 10

1701 Lys Arg Arg Gly Arg Ser Asn Ser Arg Gly Arg Lys Asn Asn Asp
 E--> 1702 20 25

1705 Ile Pro Leu Ser Phe Tyr Asn Phe Ile Thr Leu Glu Gln Glu Ser
 E--> 1706 35 40

1709 Lys Phe Trp Asn Leu Cys Pro Arg Asp Leu Val Pro Lys Gly Ile
 E--> 1710 50 55

1713 Gly Asn Lys Asp Gln Gln Ile Gly Tyr Trp Asn Arg Gln Ile Arg
 E--> 1714 65 70

1717 Tyr Arg Ile Val Lys Gly Gln Arg Lys Glu Leu Ala Glu Arg Trp
 E--> 1718 80 85

1721 Phe Phe Tyr Phe Leu Gly Thr Gly Phe His Ala Asp Ala Lys Phe
 E--> 1722 95 100

1725 Lys Asp Lys Ile Asp Gly Val Phe Trp Val Ala Arg Asp Gly Ala
 E--> 1726 110 115

1729 Met Asn Lys Pro Thr Thr Leu Gly Thr Arg Gly Thr Asn Asn Glu
 E--> 1730 125 130

1733 Ser Lys Pro Leu Arg Phe Asp Gly Lys Ile Pro Pro Gln Phe Gln
 E--> 1734

		140	145
1737	Leu Glu Val Asn Arg Ser Arg Asn Asn Ser Arg Ser Gly Ser Gln		
E--> 1738		155	160
1741	Ser Arg Ser Val Ser Arg Asn Arg Ser Gln Ser Arg Gly Arg His		
E--> 1742		170	175
1745	His Ser Asn Asn Gln Asn Asn Asn Val Glu Asp Thr Ile Val Ala		
E--> 1746		185	190
1749	Val Leu Glu Lys Leu Gly Val Thr Asp Lys Gln Arg Ser Arg Ser		
E--> 1750		200	205
1753	Lys Pro Arg Glu Arg Ser Asp Ser Lys Pro Arg Asp Thr Thr Pro		
E--> 1754		215	220

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RAW SEQUENCE LISTING

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Input Set : A:\Sequence Listing - Scott et al
 Output Set: N:\CRF3\06212001\I873881.raw

1757 Lys Asn Ala Asn Lys His Thr Trp Lys Lys Thr Ala Gly Lys Gly
 E--> 1758 230 235

1761 Asp Val Thr Thr Phe Tyr Gly Ala Arg Ser Ser Ser Ala Asn Phe
 E--> 1762 245 250

1765 Gly Asp Ser Asp Leu Val Ala Asn Gly Asn Ala Ala Lys Cys Tyr
 E--> 1766 260 265

1769 Pro Gln Ile Ala Glu Cys Val Pro Ser Val Ser Ser Ile Ile Phe
 E--> 1770 275 280

1773 Gly Ser Gln Trp Ser Ala Glu Glu Ala Gly Asp Gln Val Lys Val
 E--> 1774 290 295

1777 Thr Leu Thr His Thr Tyr Tyr Leu Pro Lys Asp Asp Ala Lys Thr
 E--> 1778 305 310

E--> 1781 Ser Gln Phe Leu Glu Gln Ile Asp Ala Tyr Lys (Atg) Pro Ser Glu 320 325

E--> 1782 335 340

1785 Val Ala Lys Asp Gln Arg Gln Arg Arg Ser Arg Ser Lys Ser Ala
 E--> 1786 340 345

1789 Asp Lys Lys Pro Glu Glu Lys Ser Val Thr Leu Val Glu Ala Tyr
 E--> 1790 350 355

1793 Thr Asp Val Phe Asp Asp Thr Gln Val Glu Met Ile Asp Glu Val
 E--> 1794 365 370

1797 Thr Asn

1798 377

1800 <210> SEQ ID NO: 25

1802 <211> LENGTH: 642 *please ensure 642 amino acids are present in the sequence*

1804 <212> TYPE: PRT

1806 <213> ORGANISM: feline leukemia virus

1808 <220> FEATURE:

1810 <223> OTHER INFORMATION:

E--> 1812 <400> SEQUENCE: ①25

1813 Met Glu Ser Pro Thr His Pro Lys Pro Ser Lys Asp Lys Thr Leu
 E--> 1814 1 5 10

1816 Ser Trp Asn Leu Ala Phe Leu Val Gly Ile Leu Phe Thr Ile Asp
 E--> 1817 20 25

1819 Ile Gly Met Ala Asn Pro Ser Pro His Gln Ile Tyr Asn Val Thr
 E--> 1820 35 40

1823 Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr

1824 50 55 60

1826 Ser Met Leu Gly Thr Leu Thr Asp Ala Tyr Pro Thr Leu His Val

1827 65 70 75

1829 Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Ile Val Leu

1830 80 85 90
E--> 1832 Asn Pro Thr Asn Val Lys His Gly Ala Arg Tyr Ser Ser Ser Lys
E--> 1833 95 100 105
1835 Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln Thr Tyr
E--> 1836 110 115 120
1838 Pro Phe Tyr Val Cys Pro Gly His Ala Pro Ser Leu Gly Pro Lys
E--> 1839 125 130 135
1841 Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
E--> 1842 140 145 150

RAW SEQUENCE LISTING
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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

1844 Gly Cys Glu Thr Thr Gly Glu Thr Trp Trp Lys Pro Thr Ser Ser
E--> 1845 155 160 165
1847 Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asp Asn Ser
E--> 1848 170 175 180
1850 Cys Glu Gly Lys Cys Asn Pro Leu Val Leu Gln Phe Thr Gln Lys
E--> 1851 185 190 195
1853 Gly Arg Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg
E--> 1854 200 205 210
1856 Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser
E--> 1857

215

220

1859 Arg Gln Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asn
E--> 1860 230 235 240
1862 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr
E--> 1863 245 250 255
1865 Gly Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala
E--> 1866 260 265 270
1868 Pro Arg Ser Val Ala Pro Thr Thr Met Gly Pro Lys Arg Ile Gly
E--> 1869 275 280 285
1871 Thr Gly Asp Arg Leu Ile Asn Leu Val Gln Gly Thr Tyr Leu Ala
E--> 1872 290 295 300
1874 Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys
E--> 1875 305 310 315
1877 Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly
E--> 1878 320 325 330
1880 Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys Leu Ser Ile
E--> 1881 335 340 345
1883 Pro Gln His Lys Leu Thr Ile Ser Glu Val Ser Gly Gln Gly Met
E--> 1884 350 355 360
1886 Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn Lys
E--> 1887 365 370 375
1889 Thr Gln Gln Gly His Thr Gly Ala His Tyr Leu Ala Ala Pro Asn
E--> 1890 380 385 390
1892 Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser
E--> 1893 395 400 405
1895 Met Ala Val Leu Asn Trp Thr Ser Asp Phe Cys Val Leu Ile Glu
E--> 1896 410 415 420
1898 Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr Val Tyr Thr
E--> 1899 425 430 435
E--> 1901 His Phe Ala Lys Ala Val Arg Phe Arg (A²⁰g) Glu Pro Ile Ser Leu
E--> 1902 440 445 450
1904 Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile Ala
E--> 1905 455 460 465
1907 Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
E--> 1908 470 475 480
1910 Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu
E--> 1911 485 490 495
1913 Glu Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser
E--> 1914 500 505 510
1916 Glu Val Val Leu Gln Asn Arg Arg Glu Leu Asp Ile Leu Phe Leu

*Mesologrid
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:37

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

E--> 1917 515 520 525
1919 Gln Glu Gly Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe
E--> 1920 530 535 540
1922 Tyr Ala Asp His Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu
E--> 1923 545 550 555
1925 Arg Glu Arg Leu Lys Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln
E--> 1926 560 565 570
1928 Gly Trp Phe Glu Gly Trp Phe Asn Lys Ser Pro Trp Phe Thr Thr
E--> 1929 575 580 585
1931 Leu Ile Ser Ser Ile Met Gly Pro Leu Leu Ile Leu Leu Leu Ile
E--> 1932 590 595 600
1934 Leu Leu Phe Gly Pro Cys Ile Leu Asn Arg Leu Val Gln Phe Val
E--> 1935 Injabs 605 610 615
E--> 1937 Lys Asp (Asg) Ile Ser Val Val Gln Ala Leu Ile Leu Thr Gln Gln
E--> 1938 620 625 630
1940 Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp Arg Pro
E--> 1941 635 640

rgt
Please Note:

Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:38

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:31 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:35 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:47 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:53 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:65 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:85 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:101 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:105 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:109 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:121 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:125 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:141 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:157 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:161 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:224 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:1
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/873,881

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Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0
 L:310 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:391 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:1
 L:392 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:3
 L:392 M:252 E: No. of Seq. differs, <211>LENGTH:Input:44 Found:40 SEQ:3
 L:406 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:4 differs:1
 L:418 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:422 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:5 differs:1
 L:434 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:438 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:6 differs:1
 L:455 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:7 differs:1
 L:645 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:649 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:8 differs:1
 L:670 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:674 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:1
 L:694 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:698 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:10 differs:1
 L:710 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:714 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:11 differs:1
 L:726 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:730 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:12 differs:1
 L:742 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:746 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:1
 L:758 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:762 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:14 differs:1
 L:774 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:778 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:15 differs:1
 L:790 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
 L:794 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:16 differs:1
 L:811 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:17 differs:1
 L:851 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:898 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:18 differs:1
 L:984 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1016 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:19 differs:1
 L:1017 M:254 E: No. of Bases conflict, LENGTH:Input:50 Counted:51 SEQ:19
 L:1017 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
 M:254 Repeated in SeqNo=19
 L:1139 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1185 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:1
 L:1190 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:2
 L:1196 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1979 Found:1980 SEQ:19
 L:1211 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:20 differs:1
 L:1213 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
 M:332 Repeated in SeqNo=20
 L:1268 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/873,881

DATE: 06/21/2001
TIME: 17:28:38

Input Set : A:\Sequence Listing - Scott et al
Output Set: N:\CRF3\06212001\I873881.raw

L:1348 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:21 differs:1
L:1350 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=21
L:1414 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1479 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:22 differs:1
L:1481 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=22
L:1628 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:23 differs:1
L:1630 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=23
L:1656 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1696 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:24 differs:1
L:1698 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=24
L:1781 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1812 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:25 differs:1
L:1814 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
M:332 Repeated in SeqNo=25
L:1832 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:1901 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1937 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:1941 M:252 E: No. of Seq. differs, <211>LENGTH:Input:642 Found:641 SEQ:25